



1-1

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	CAGTACAATC	TGCTCTGATG	CCGCATAGTT
80	90	100	110	120	130	140
*	*	*	*	*	*	*
AAGCCAGTAT	CTGCTCCCTG	CTTGTGTGTT	GGAGGTCGCT	GAGTAGTGCG	CGAGCAAAT	TTAAGCTACA
150	160	170	180	190	200	210
*	*	*	*	*	*	*
ACAAGGCAAG	GCTTGACCGA	CAATTGCATG	AAGAACATGC	TTAGGGTTAG	GCGTTTGCG	CTGCTTCGCG
220	230	240	250	260	270	280
*	*	*	*	*	*	*
ATGTACGGGC	CAGATATAACG	CGTTGACATT	GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC
290	300	310	320	330	340	350
*	*	*	*	*	*	*
ATTAGTTCAT	AGCCCATATA	TGGAGTTCCG	CGTTACATAA	CTTACGGTA	ATGGCCCGCC	TGGCTGACCG
360	370	380	390	400	410	420
*	*	*	*	*	*	*
CCCAACGACC	CCCGCCCAT	GACGTCAATA	ATGACGTATG	TTCCCATAAGT	AACGCCAATA	GGGACTTTCC
430	440	450	460	470	480	490
*	*	*	*	*	*	*
ATTGACGTCA	ATGGGTGGAC	TATTTACGGT	AAACTGCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC
500	510	520	530	540	550	560
*	*	*	*	*	*	*
AAGTACGCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCAGTA	CATGACCTTA
570	580	590	600	610	620	630
*	*	*	*	*	*	*
TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC	CATGGTGATG	CGGTTTGGC
640	650	660	670	680	690	700
*	*	*	*	*	*	*
AGTACATCAA	TGGGCGTGG	TAGCGGTTTG	ACTCACGGGG	ATTCCAAGT	CTCCACCCCA	TTGACGTCAA
710	720	730	740	750	760	770
*	*	*	*	*	*	*
TGGGAGTTG	TTTGGCACC	AAAATCAACG	GGACTTTCCA	AAATGTCGTA	ACAACTCCGC	CCCATTGACG
780	790	800	810	820	830	840
*	*	*	*	*	*	*
CAAATGGGCG	GTAGGCCTGT	ACGGTGGGAG	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA
850	860	870	880	890	900	910
*	*	*	*	*	*	*
CTGCTTAACT	GGCTTATCGA	AATTAATACG	ACTCACTATA	GGGAGACCCA	AGCTTCGCGAG	AATTCTGCG
920	930	940	950	960	970	980
*	*	*	*	*	*	*
GCTGCTACAG	TGTGTCCAGC	GTCCTGCCCTG	GCTGTGCTGA	GCGCTGGAAC	AGTGGCGCAT	CATTCAAGTG
990	1000	1010	1020	1030	1040	1050
*	*	*	*	*	*	*
CACAGTTACC	CATCCTGAGT	CTGGCACCTT	AACTGGCACA	ATTGCCAAAG	TCACAGGTGA	GCTCAGATGC
1060	1070	1080	1090	1100	1110	1120
*	*	*	*	*	*	*
ATACCAGGAC	ATTGTATGAC	GTTCCCTGCT	CACATGCCTG	CTTCTTCCT	ATAATACAGA	TGCTCAACTA
1130	1140	1150	1160	1170	1180	1190
*	*	*	*	*	*	*
ACTGCTCATG	TCCTTATATC	ACAGAGGGAA	ATTGGAGCTA	TCTGAGGAAC	TGCCCAGAAG	GGAAGGGCAG

FIG. 1-2

1200	1210	1220	1230	1240	1250	1260
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AGGGGTCTTG CTCTCCTTGT CTGAGCCATA ACTCTTCTTT CTACCTTCCA GTGAACACCT TCCCCACCCCA						
1270	1280	1290	1300	1310	1320	1330
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
GGTCCACCTG CTACCGCCGC CGTCGGAGGA GCTGGCCCTG AATGAGCTCT TGTCCCTGAC ATGCCTGGTG						
1340	1350	1360	1370	1380	1390	1400
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
CGAGCTTCA ACCCTAAAGA AGTGCTGGTG CGATGGCTGC ATGGAAATGA GGAGCTGTCC CCAGAAAGCT						
1410	1420	1430	1440	1450	1460	1470
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
ACCTAGTGTT TGAGCCCCTA AAGGAGCCAG GCGAGGGAGC CACCACCTAC CTGGTGACAA GCGTGTGCG						
1480	1490	1500	1510	1520	1530	1540
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
TGTATCAGCT GAAAGCTTGA TATCGAATTG CGGAGGCCGA ACCGGCAGTG CAGCCCCAAG CCCCCCAGTC						
1550	1560	1570	1580	1590		
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *		
CCCGAGCACG CGTGGGCC ATG CGT CCC CTG CGC CCC CGC GCC GCG CTG CTG GCG CTC CTG						
		Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu				
1600	1610	1620	1630	1640	1650	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
GCC TCG CTC CTG GCC GCG CCC CCG GTG GCC CCG GCC GAG GCG CCG CAC CTG GTG CAT						
Ala Ser Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His						
1660	1670	1680	1690	1700	1710	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
GTG GAC GCG GCC CGC GCG CTG TGG CCC CTG CGG CGC TTC TGG AGG AGC ACA GGC TTC						
Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe						
1720	1730	1740	1750	1760	1770	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
TGC CCC CCG CTG CCA CAC AGC CAG GCT GAC CAG TAC GTC CTC AGC TGG GAC CAG CAG						
Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln						
1780	1790	1800	1810	1820		
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *		
CTC AAC CTC GCC TAT GTG GGC GCC GTC CCT CAC CGC GGC ATC AAG CAG GTC CGG ACC						
Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr						
1830	1840	1850	1860	1870	1880	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *		
CAC TGG CTG CTG GAG CTT GTC ACC ACC AGG GGG TCC ACT GGA CGG GGC CTG AGC TAC						
His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr						
1890	1900	1910	1920	1930	1940	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
AAC TTC ACC CAC CTG GAC GGG TAC CTG GAC CTT CTC AGG GAG AAC CAG CTC CTC CCA						
Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro						
1950	1960	1970	1980	1990		
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *		
GGG TTT GAG CTG ATG GGC AGC GCC TCG GGC CAC TTC ACT GAC TTT GAG GAC AAG CAG						
Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln						

FIG. 1-3

2000	2010	2020	2030	2040	2050
*	*	*	*	*	*
CAG	G TG	T TT	G AG	G A G	T G G
Gln	Val	Phe	Glu	Trp	Lys
2060	2070	2080	2090	2100	2110
*	*	*	*	*	*
TAC	GGA	CTG	GCG	CAT	GTT
Tyr	Gly	Leu	Ala	His	Val
2120	2130	2140	2150	2160	
*	*	*	*	*	*
CAC	GAC	TTT	GAC	AAC	GTC
His	Asp	Phe	Asp	Asn	Val
2170	2180	2190	2200	2210	2220
*	*	*	*	*	*
TGC	TCG	GAG	GGT	CTG	CGC
Cys	Ser	Glu	Gly	Leu	Arg
2230	2240	2250	2260	2270	2280
*	*	*	*	*	*
TCC	TTC	CAC	ACC	CCA	CCG
Ser	Phe	His	Thr	Pro	Arg
2290	2300	2310	2320	2330	2340
*	*	*	*	*	*
GAC	GGT	ACC	AAC	TTC	TTC
Asp	Gly	Thr	Asn	Phe	Thr
2350	2360	2370	2380	2390	
*	*	*	*	*	*
CAC	AGG	AAG	GGT	GCG	CGC
His	Arg	Lys	Gly	Ala	Arg
2400	2410	2420	2430	2440	2450
*	*	*	*	*	*
CAG	CAG	ATC	CGG	CAG	CTC
Gln	Gln	Ile	Arg	Gln	Leu
2460	2470	2480	2490	2500	2510
*	*	*	*	*	*
GCG	GAC	CCG	CTG	GTC	GGC
Ala	Asp	Pro	Leu	Val	Gly
2520	2530	2540	2550	2560	
*	*	*	*	*	*
GCG	GCC	ATG	GTG	GTG	AAG
Ala	Ala	Met	Val	Val	Val
2570	2580	2590	2600	2610	2620
*	*	*	*	*	*
ACC	TCC	GCC	TTC	CCC	TAC
Thr	Ser	Ala	Phe	Pro	Tyr
2630	2640	2650	2660	2670	2680
*	*	*	*	*	*
CCG	CAC	CCC	TTC	GCG	CAG
Pro	His	Pro	Phe	Ala	Gln
2690	2700	2710	2720	2730	2740
*	*	*	*	*	*

FIG. 1-4

2690	2700	2710	2720	2730	
*	*	*	*	*	
CCG CCG CAC GTG CAG CTG TTG CGC AAG CCG GTG CTC ACG GCC ATG GGG CTG CTG GCG					
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala					
2740	2750	2760	2770	2780	2790
*	*	*	*	*	*
CTG CTG GAT GAG GAG CAG CTC TGG GCC GAA GTG TCG CAG GCC GGG ACC GTC CTG GAC					
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp					
2800	2810	2820	2830	2840	2850
*	*	*	*	*	*
AGC AAC CAC ACG GTG GGC GTC CTG GCC AGC GCC CAC CGC CCC CAG GGC CCG GCC GAC					
Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp					
2860	2870	2880	2890	2900	2910
*	*	*	*	*	*
GCC TGG CGC GCC GCG GTG CTG ATC TAC GCG AGC GAC GAC ACC CGC GCC CAC CCC AAC					
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn					
2920	2930	2940	2950	2960	
*	*	*	*	*	
CGC AGC GTC GCG GTG ACC CTG CGG CTG CGC GGG GTG CCC CCC GGC CCG GGC CTG GTC					
Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val					
2970	2980	2990	3000	3010	3020
*	*	*	*	*	*
TAC GTC ACG CGC TAC CTG GAC AAC GGG CTC TGC AGC CCC GAC GGC GAG TGG CGG CGC					
Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg					
3030	3040	3050	3060	3070	3080
*	*	*	*	*	*
CTG GGC CGG CCC GTC TTC CCC ACG GCA GAG CAG TTC CGG CGC ATG CGC GCG GCT GAG					
Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu					
3090	3100	3110	3120	3130	
*	*	*	*	*	
GAC CCG GTG GCC GCG GCG CCC CGC CCC TTA CCC GCC GGC GGC CGC CTG ACC CTG CGC					
Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg					
3140	3150	3160	3170	3180	3190
*	*	*	*	*	*
CCC GCG CTG CGG CTC CCG TCG CTT TTG CTG GTG CAC GTG TGT GCG CGC CCC GAG AAG					
Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys					
3200	3210	3220	3230	3240	3250
*	*	*	*	*	*
CCG CCC GGG CAG GTC ACG CGG CTC CGC GCC CTG CCC CTG ACC CAA GGG CAG CTG GTT					
Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val					
3260	3270	3280	3290	3300	
*	*	*	*	*	
CTG GTC TGG TCG GAT GAA CAC GTG GGC TCC AAG TGC CTG TGG ACA TAC GAG ATC CAG					
Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln					
3310	3320	3330	3340	3350	3360
*	*	*	*	*	*
TTC TCT CAG GAC GGT AAG GCG TAC ACC CCG GTC AGC AGG AAG CCA TCG ACC TTC AAC					
Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn					

FIG. 1-5

3370	3380	3390	3400	3410	3420
*	*	*	*	*	*
CTC TTT GTG TTC AGC CCA GAC ACA GGT GCT GTC TCT GGC TCC TAC CGA GTT CGA GCC					
Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala					
3430	3440	3450	3460	3470	3480
*	*	*	*	*	*
CTG GAC TAC TGG GCC CGA CCA GGC CCC TTC TCG GAC CCT GTG CCG TAC CTG GAG GTC					
Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val					
3490	3500	3510	3520	3530	3540
*	*	*	*	*	*
CCT GTG CCA AGA GGG CCC CCA TCC CCG GGC AAT CCA TGAG CCTGTGCTGA GCCCCAGTGG					
Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro					
3550	3560	3570	3580	3590	3600
*	*	*	*	*	*
GTTCGACCTC CACCGGCAGT CAGCGAGCTG GGGCTGCACT GTGCCCATGC TGCCCTCCCA TCACCCCCCTT					
3620	3630	3640	3650	3660	3670
*	*	*	*	*	*
TGCAATATAT TTTTATATTAA TAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA					
3690	3700	3710	3720	3730	3740
*	*	*	*	*	*
AAAAAAAAAA AAAAAAAAAG AATTCTCTGA GCCCGGGGGA TCCACTAGTT CTAGAGGGCC CGTTAAACC					
3760	3770	3780	3790	3800	3810
*	*	*	*	*	*
CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTG CCCCTCCCCC GTGCCTTCCT					
3830	3840	3850	3860	3870	3880
*	*	*	*	*	*
TGACCCCTGGA AGGTGCCACT CCCACTGTCC TTTCTTAATA AAATGAGGAA ATTGCATCGC ATTGTCTGAG					
3900	3910	3920	3930	3940	3950
*	*	*	*	*	*
TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACAATAGC					
3970	3980	3990	4000	4010	4020
*	*	*	*	*	*
AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGGC TCGAGAGCTT					
4040	4050	4060	4070	4080	4090
*	*	*	*	*	*
GGCGTAATCA TGGTCATAGC TGTTTCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA					
4110	4120	4130	4140	4150	4160
*	*	*	*	*	*
GCCGGAAGCA TAAAGTGTAA AGCCTGGGGT GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTGCCT					
4180	4190	4200	4210	4220	4230
*	*	*	*	*	*
CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG					
4250	4260	4270	4280	4290	4300
*	*	*	*	*	*
AGGCGGTTG CGTATTGGGC GCTTTCCGC TTCCCTGCTC ACTGACTCGC TGCGCTCGGT CGTTCGGCTG					
4320	4330	4340	4350	4360	4370
*	*	*	*	*	*
CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGAT AACGCAGGAA					

FIG. 1-6

4390	4400	4410	4420	4430	4440	4450
*	*	*	*	*	*	*
AGAACATGTG	AGCAAAAGGC	CAGCAAAGG	CCAGGAACCG	TAAAAAGGCC	GCGTTGCTGG	CGTTTTCCA
4460	4470	4480	4490	4500	4510	4520
*	*	*	*	*	*	*
TAGGCTCCGC	CCCCCTGACG	AGCATCACAA	AAATCGACGC	TCAAGTCAGA	GGTGGCGAAA	CCCGACAGGA
4530	4540	4550	4560	4570	4580	4590
*	*	*	*	*	*	*
CTATAAAGAT	ACCAGGC GTT	TCCCCCTGG	AGCTCCCTCG	TGCGCTCTCC	TGTTCCGACC	CTGCCGCTTA
4600	4610	4620	4630	4640	4650	4660
*	*	*	*	*	*	*
CCGGATACCT	GTCCGCCTT	CTCCCTTCGG	GAAGCGTGGC	GCTTCTCAA	TGCTCACGCT	GTAGGTATCT
4670	4680	4690	4700	4710	4720	4730
*	*	*	*	*	*	*
CAGTCGGTG	TAGTCGTTC	GCTCCAAGCT	GGGCTGTGTG	CACGAACCCC	CCGTT CAGCC	CGACCGCTGC
4740	4750	4760	4770	4780	4790	4800
*	*	*	*	*	*	*
GCCTTATCCG	GTAACTATCG	TCTTGAGTCC	AACCCGGTAA	GACACGACTT	ATGCCCACTG	GCAGCAGCCA
4810	4820	4830	4840	4850	4860	4870
*	*	*	*	*	*	*
CTGGTAACAG	GATTAGCAGA	GCGAGGTATG	TAGGCGGTGC	TACAGAGTTC	TTGAAGTGGT	GGCCTAACTA
4880	4890	4900	4910	4920	4930	4940
*	*	*	*	*	*	*
CGGCTACACT	AGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT
4950	4960	4970	4980	4990	5000	5010
*	*	*	*	*	*	*
GGTAGCTCTT	GATCCGGCAA	ACAAACCAC	GCTGGTAGCG	GTGGTTTTT	TGTTTGCAAG	CAGCAGATTA
5020	5030	5040	5050	5060	5070	5080
*	*	*	*	*	*	*
CGCGCAGAAA	AAAAGGATCT	CAAGAAGATC	CTTGTACCTT	TTCTACGGGG	TCTGACGCTC	AGTGGAACGA
5090	5100	5110	5120	5130	5140	5150
*	*	*	*	*	*	*
AAACTCACGT	TAAGGGATT	TGGTCATGAG	ATTATCAAAA	AGGATCTTCA	CCTAGATCCT	TTAAATTAA
5160	5170	5180	5190	5200	5210	5220
*	*	*	*	*	*	*
AAATGAAGTT	TTAAATCAAT	CTAAAGTATA	TATGAGTAAA	CTTGGTCTGA	CAGTTACCAA	TGCTTAATCA
5230	5240	5250	5260	5270	5280	5290
*	*	*	*	*	*	*
GTGAGGCACC	TATCTCAGCG	ATCTGTCTAT	TTCTGTTCATC	CATAGTTGCC	TGACTCCCCG	TCGTGTAGAT
5300	5310	5320	5330	5340	5350	5360
*	*	*	*	*	*	*
AACTACGATA	CGGGAGGGCT	TACCATCTGG	CCCCAGTGCT	GCAATGATAC	CGCGAGACCC	ACGETCACCG
5370	5380	5390	5400	5410	5420	5430
*	*	*	*	*	*	*
GCTCCAGATT	TATCAGCAAT	AAACCAGCCA	GCCGGAAGGG	CCGAGCGCAG	AAGTGGTCCT	GCAACTTTAT
5440	5450	5460	5470	5480	5490	5500
*	*	*	*	*	*	*
CCGCCTCCAT	CCAGTCTATT	AATTGTTGCC	GGGAAGCTAG	AGTAAGTAGT	TCGCCAGTTA	ATAGTTGCG

FIG. 1-7

5510	5520	5530	5540	5550	5560	5570
*	*	*	*	*	*	*
CAACGTTGTT	GCCATTGCTA	CAGGCATCGT	GGTGTACAGC	TCGTCGTTG	GTATGGCTTC	ATTAGCTCC
5580	5590	5600	5610	5620	5630	5640
*	*	*	*	*	*	*
GGTTCCAAAC	GATCAAGGCG	AGTTACATGA	TCCCCCATGT	TGTGCAAAA	AGCGGTTAGC	TCCTTCGGTC
5650	5660	5670	5680	5690	5700	5710
*	*	*	*	*	*	*
CTCCGATCGT	TGTCAGAACT	AAGTTGGCCG	CAGTGTATC	ACTCATGGTT	ATGGCAGCAC	TGCATAATT
5720	5730	5740	5750	5760	5770	5780
*	*	*	*	*	*	*
TCTTACTGTC	ATGCCATCCG	TAAGATGCTT	TTCTGTGACT	GGTGAGTACT	CAACCAAGTC	ATTCTGAGAA
5790	5800	5810	5820	5830	5840	5850
*	*	*	*	*	*	*
TAGTGTATGC	GGCGACCGAG	TTGCTCTTGC	CCGGCGTCAA	TACGGGATAA	TACCGCGCCA	CATAGCAGAA
5860	5870	5880	5890	5900	5910	5920
*	*	*	*	*	*	*
CTTTAAAAGT	GCTCATCATT	GGAAAACGTT	CTTCGGGGCG	AAAACCTCTCA	AGGATCTTAC	CGCTGTTGAG
5930	5940	5950	5960	5970	5980	5990
*	*	*	*	*	*	*
ATCCAGTTCG	ATGTAACCCA	CTCGTGCACC	CAACTGATCT	TCAGCATCTT	TTACTTCAC	CAGCGTTCT
6000	6010	6020	6030	6040	6050	6060
*	*	*	*	*	*	*
GGGTGAGCAA	AAACAGGAAG	GCAAAATGCC	GCAAAAAAGG	GAATAAGGGC	GACACGGAAA	TGTTGAATAC
6070	6080	6090	6100	6110	6120	6130
*	*	*	*	*	*	*
TCATACTCTT	CCTTTTTCAA	TATTATTGAA	GCATTATCA	GGGTTATTGT	CTCATGAGCG	GATACATATT
6140	6150	6160	6170	6180	6190	6200
*	*	*	*	*	*	*
TGAATGTATT	TAGAAAAATA	AACAAATAGG	GGTCCGCGC	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC

Fig. 2A

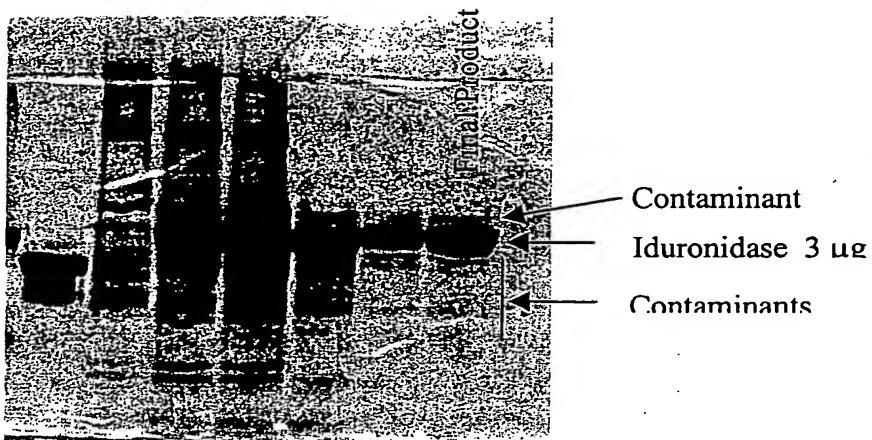
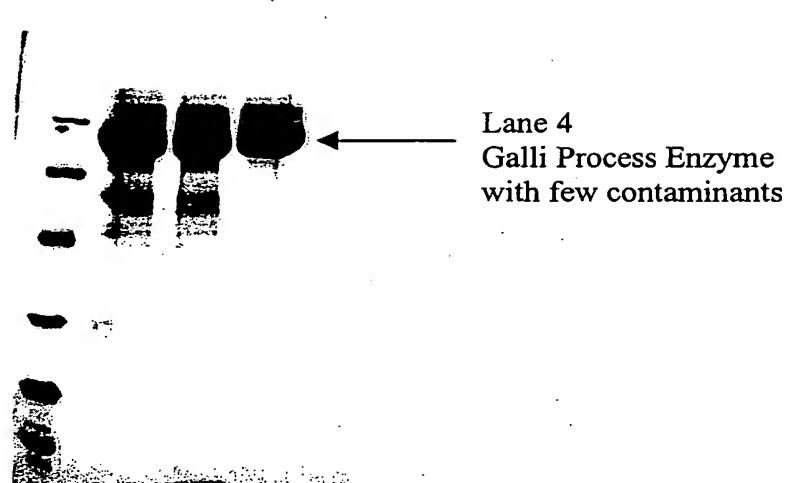


Fig. 2B



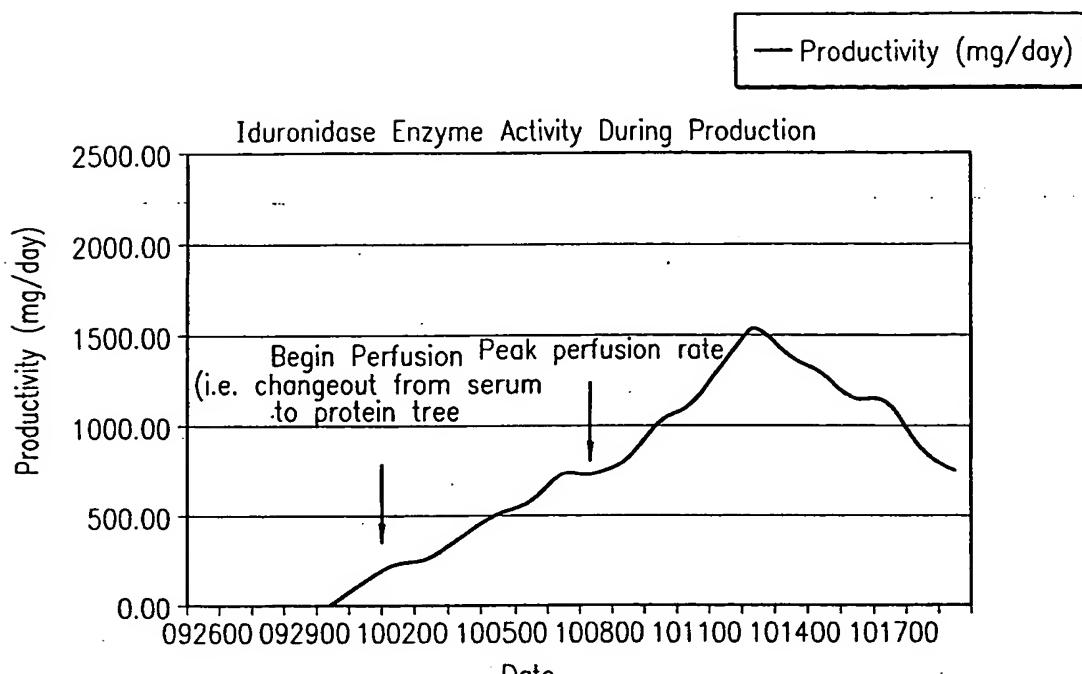


FIG. 3A

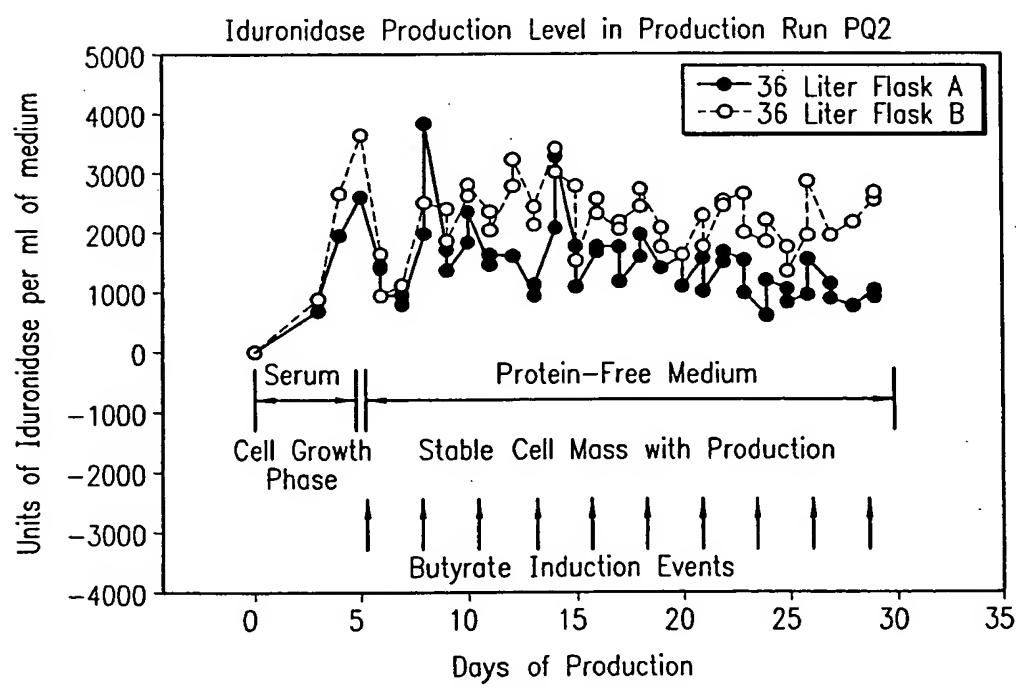
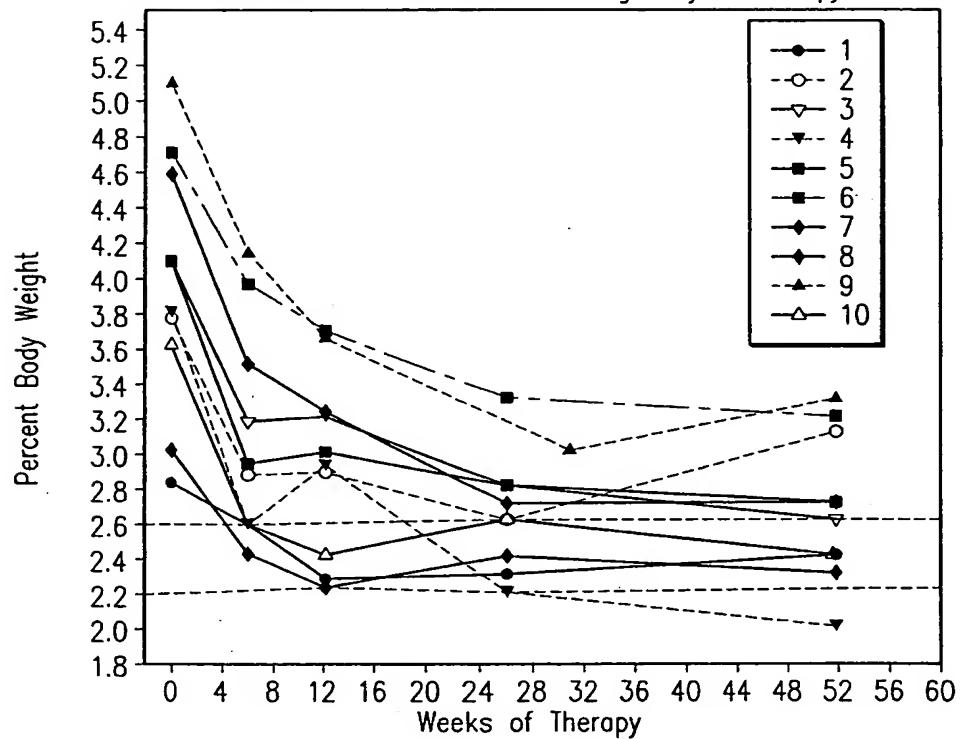


FIG. 3B

FIG. 4 Reduction in Liver Volume During Enzyme Therapy



Urinary GAG Excretion During Enzyme Therapy

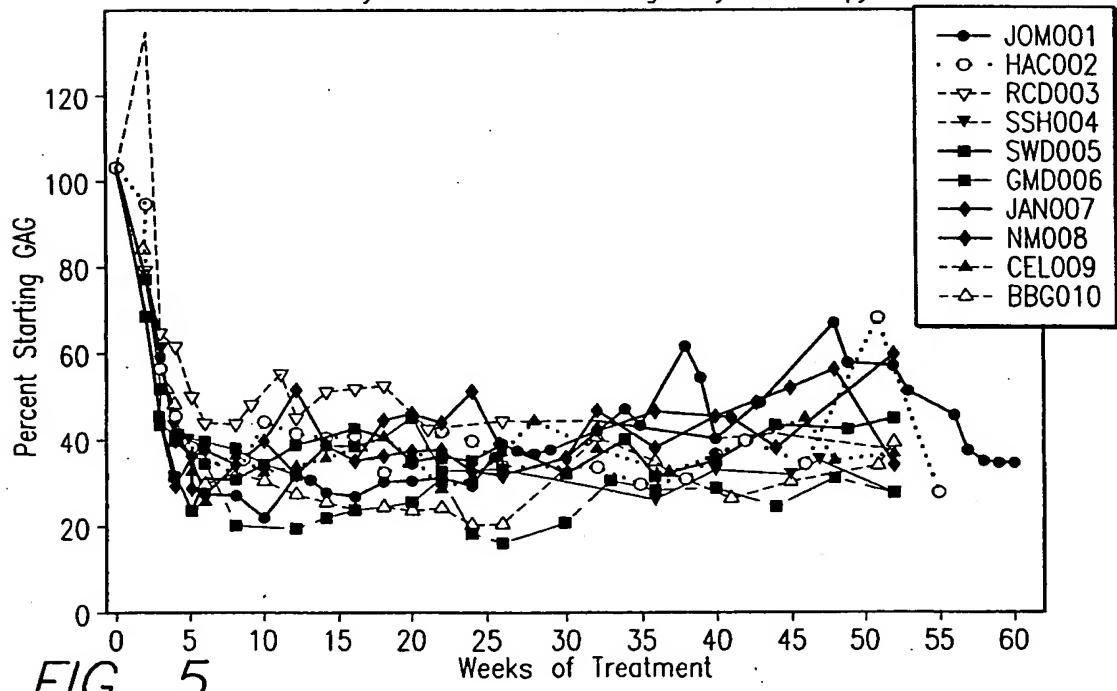
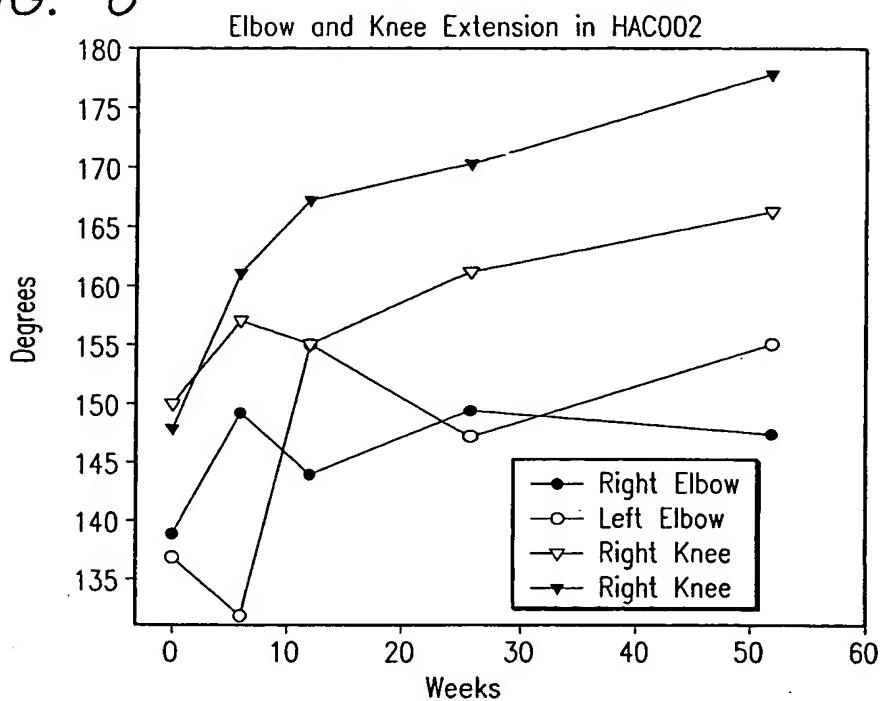


FIG. 5

FIG. 6



Shoulder flexion to 104 weeks in four patients with most restriction

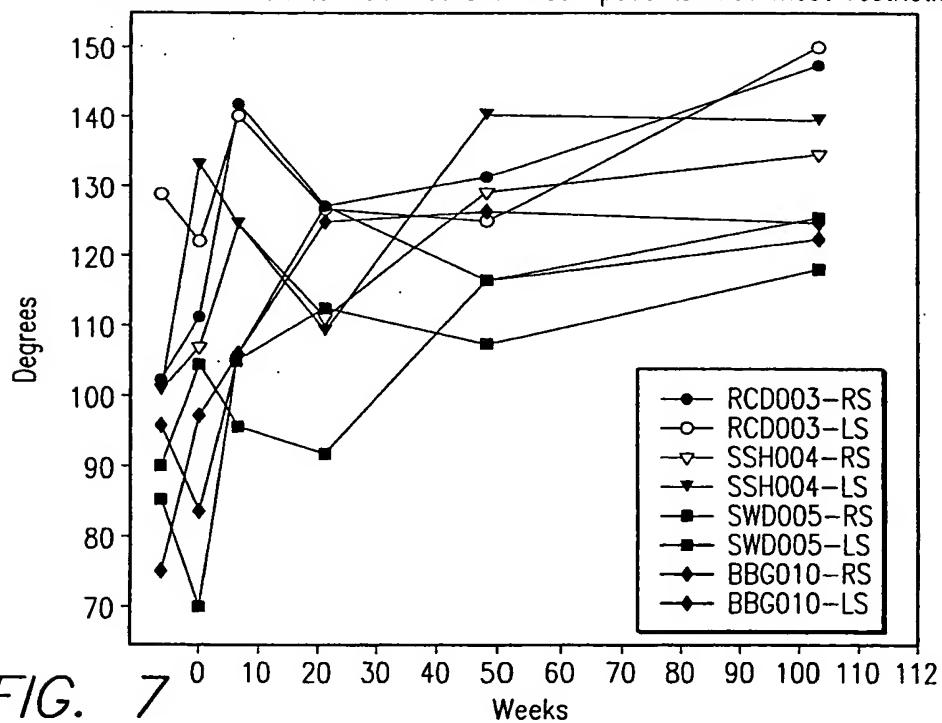


FIG. 7

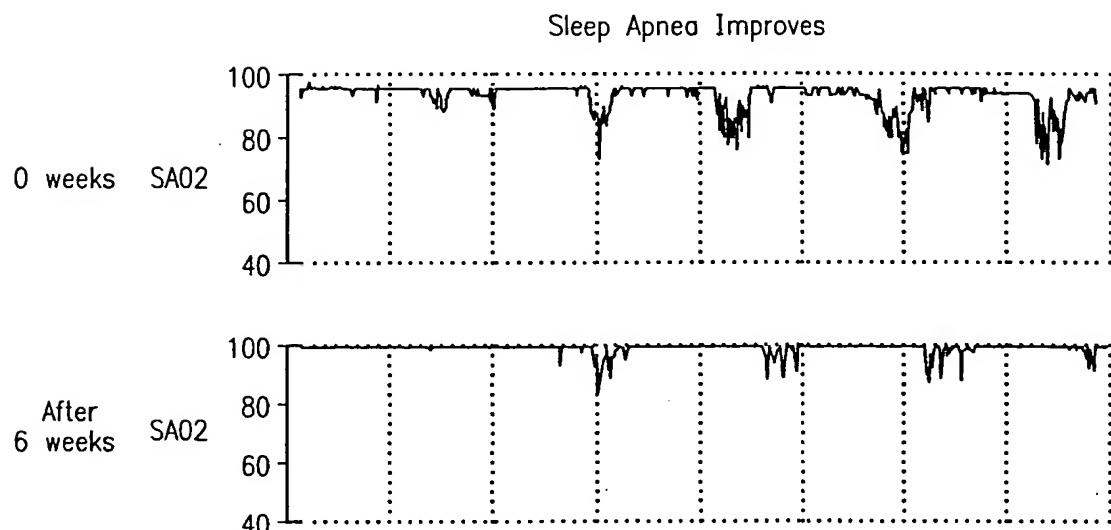


FIG. 8

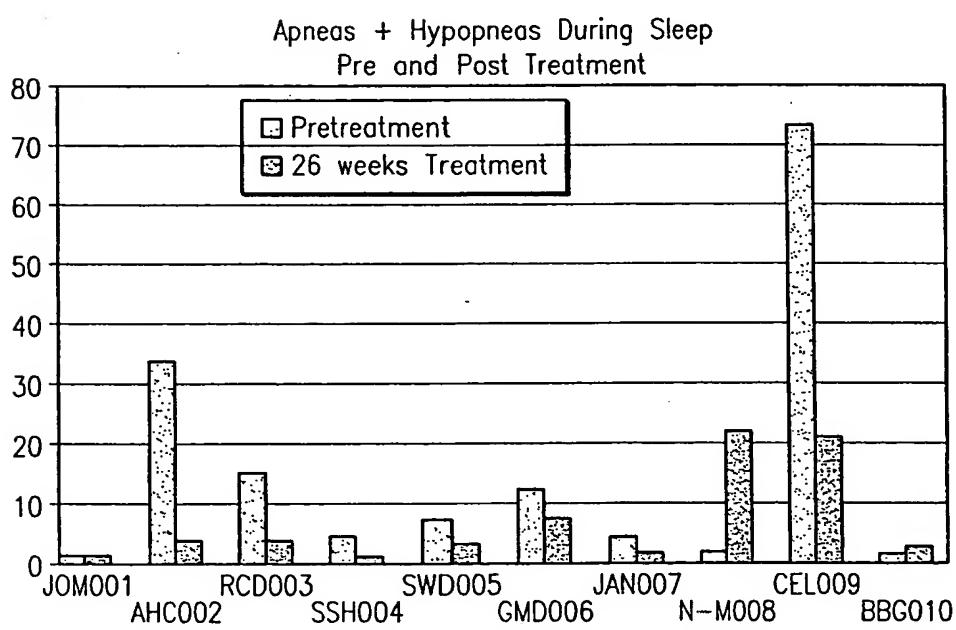


FIG. 9

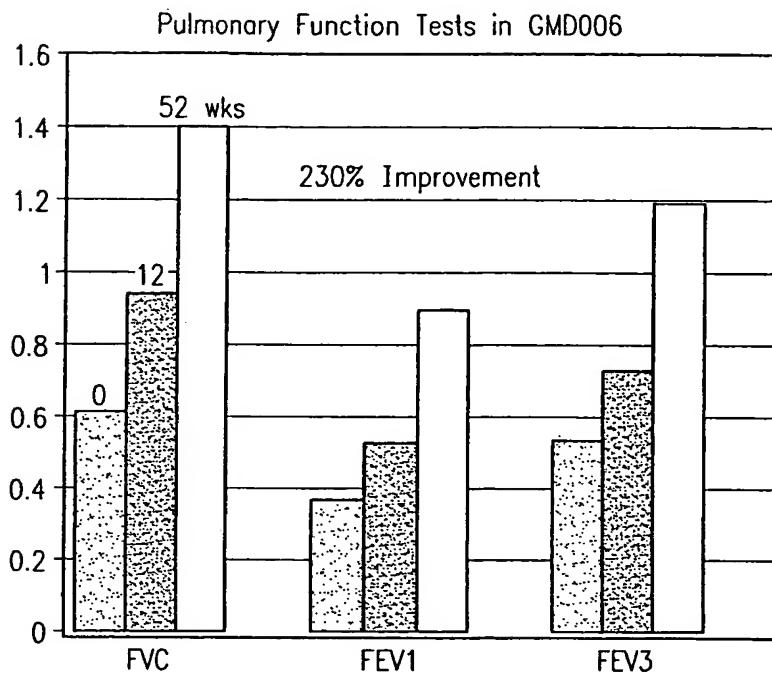


FIG. 10

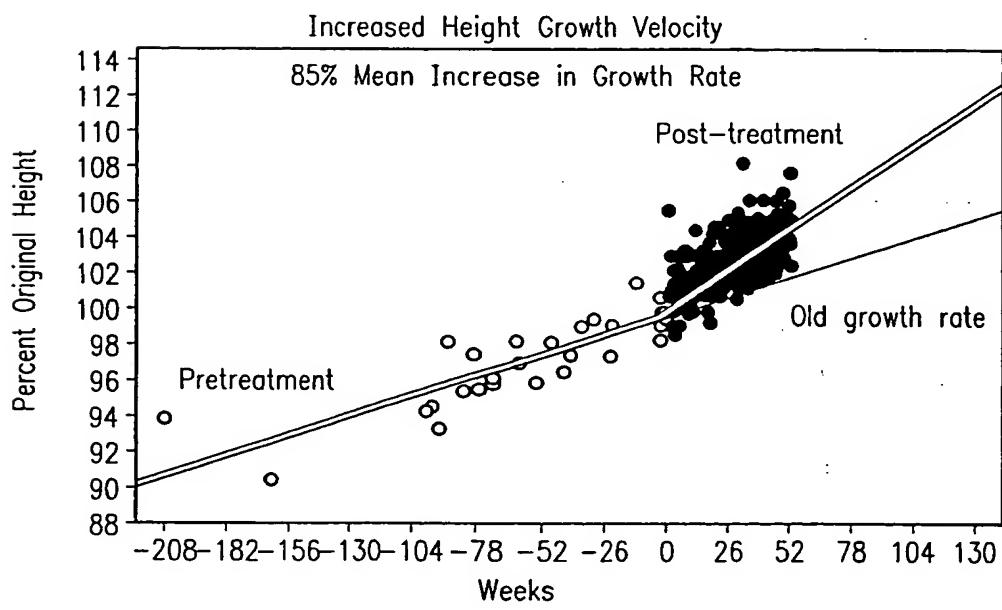


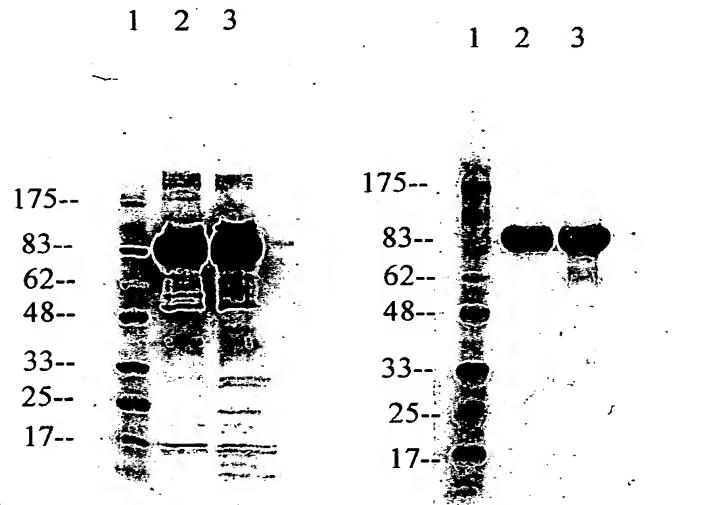
FIG. 11

FIG. 12

Chinese Hamster Ovary Host Protein Contamination by ELISA Assay

SOURCE AND BATCH NUMBER	CHOP PROTEIN CONTAMINATION (microgram per milligram)	PERCENT CHOP CONTAMINATION	PURITY OF THE ENZYME FROM CHOP
Prior Process (Carson/REI)			
C9002	14	1.4%	98.6%
C9003	24	2.4%	97.6%
C9004	16	1.6%	98.4%
New Process (Galli)			
P1003	<1.3	<0.13%	>99.9%
P1006	1.2	0.12%	99.9%
P1007	<0.6	<0.06%	>99.9%
P1008	<0.67	<0.067%	>99.9%

Comparison of Galli and Carson Material



1 Marker
2 Galli Referenced-0201
3 Carson C9002

5ug/lane

FIG. 13